

50					55					60					
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
65					70					75					80
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu
				85					90					95	
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val
			100					105					110		
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val
		115					120					125			
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu
	130					135					140				
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu
145				150					155						160
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp
			165					170						175	
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln
			180					185					190		
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu
	195						200					205			
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly
	210						215					220			
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr
225				230					235					240	
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met
			245					250						255	
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys
			260					265					270		
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro
		275					280					285			
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu
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<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence: pks chimera

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 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe

48

1	5	10	15	
gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag				96
Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	20	25	30	
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa				144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	35	40	45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat				192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	50	55	60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag				240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	65	70	75	80
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag				288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	85	90	95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg				336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	100	105	110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc				384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	115	120	125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa				432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	130	135	140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta				480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	145	150	155	160
aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac				528
Lys Val Leu Lys Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	165	170	175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa				576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	180	185	190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag				624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	195	200	205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg				672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	210	215	220	
ccc tat gac aaa ggc gag tac tgc ccc tct gtc cag aag aca ctc tat				720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	225	230	235	240
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg				768
Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met	245	250	255	
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa				816

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270

atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca 864
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

tga 915

305

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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220